WEST Search History

Hide Items | Restore | Clear | Cancel

DATE: Friday, April 15, 2005

Hide?	Set Name	Query	Hit Count
	DB=USPT,USOC,EPAB,JPAB,DWPI; THES=ASSIGNEE; PLUR=YES; OP=ADJ		
☐	L12	phosphatase same aerogenes	13
	DB=PGPB; THES=ASSIGNEE; PLUR=YES; OP=ADJ		
☐	L11	phosphatase same aerogenes	7
	DB=USPT,USOC,EPAB,JPAB,DWPI,TDBD; THES=ASSIGNEE; PLUR=YES; OP=ADJ		
☐	L10	L9 and mut$10	11
☐	L9	phosphatase same aerogenes	13
☐	L8	L7 and muta$10	214
☐	L7	phosphatase and aerogenes	322
☐	L6	phosphatase and blattae	10
	DB=PGPB; THES=ASSIGNEE; PLUR=YES; OP=ADJ		
☐	L5	phosphatase and blattae	12
☐	L4	phosphatase and crystal$7 and blattae	0
	DB=USPT,USOC,EPAB,JPAB,DWPI; THES=ASSIGNEE; PLUR=YES; OP=ADJ		
☐	L3	phosphatase and crystal$7 and blattae	0
☐	L2	(phosphatase same crystal$7) and blattae	0
☐	L1	(phosphatase same crystal) and blattae	0

END OF SEARCH HISTORY

STN SEARCH **09/807,990**

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FILE 'HOME' ENTERED AT 10:40:05 ON 15 APR 2005
=> file .nash
=> s phosphatase and blattae and crystal?
L1            2 FILE MEDLINE
L2            4 FILE CAPLUS
L3            2 FILE SCISEARCH
L4            1 FILE LIFESCI
L5            2 FILE BIOSIS
L6            2 FILE EMBASE

TOTAL FOR ALL FILES
L7           13 PHOSPHATASE AND BLATTAE AND CRYSTAL?

=> dup rem l7
PROCESSING COMPLETED FOR L7
L8             4 DUP REM L7 (9 DUPLICATES REMOVED)

=> d ibib abs

L8   ANSWER 1 OF 4  CAPLUS  COPYRIGHT 2005 ACS on STN
ACCESSION NUMBER:         2002:19321  CAPLUS Full-text
DOCUMENT NUMBER:          136:84776
TITLE:                    Enzymic method of nucleoside-5'-phosphate
INVENTOR(S):              Iida, Iwao; Arashida, Takaki; Abe, Shigemitsu
PATENT ASSIGNEE(S):       Ajinomoto Co., Inc., Japan
SOURCE:                   Jpn. Kokai Tokkyo Koho, 10 pp.
                          CODEN: JKXXAF
DOCUMENT TYPE:            Patent
LANGUAGE:                 Japanese
FAMILY ACC. NUM. COUNT:   1
PATENT INFORMATION:

     PATENT NO.           KIND   DATE        APPLICATION NO.         DATE
     ---------------      ----   --------    --------------------    --------
     JP 2002000289         A2    20020108    JP 2000-189226          20000623
PRIORITY APPLN. INFO.:                       JP 2000-189226          20000623
OTHER SOURCE(S):          CASREACT 136:84776
AB     Nucleosides, especially low-solubility nucleosides, or their precursor crystal is phys.
       pulverized to a size having sp. surface area of 0.4 m2/g, incubated with enzyme such as
       acidic phosphatase in the presence of an phosphate donor to prepare nucleoside-5'-
       phosphate. Manufacture of 5'-guanylic acid from guanosine crystal in the presence of
       pyrophosphoric acid with acidic phosphatase mutant of Escherichia blattae was shown.



=> d ibib abs 2-4

L8   ANSWER 2 OF 4     MEDLINE on STN                    DUPLICATE 1
ACCESSION NUMBER:   2002471678     MEDLINE Full-text
DOCUMENT NUMBER:    PubMed ID: 12200535
TITLE:              Enhancement of nucleoside phosphorylation activity in an
                    acid phosphatase.
AUTHOR:             Ishikawa Kohki; Mihara Yasuhiro; Shimba Nobuhisa; Ohtsu
                    Naoko; Kawasaki Hisashi; Suzuki Ei-ichiro; Asano Yasuhisa
CORPORATE SOURCE:   Central Research Laboratories, Ajinomoto Co., Inc., 1-1
                    Suzuki-cho Kawasaki-ku, Kawasaki 210-868, Japan.
SOURCE:             Protein engineering, (2002 Jul) 15 (7) 539-43.
                    Journal code: 8801484. ISSN: 0269-2139.
PUB. COUNTRY:       England: United Kingdom
DOCUMENT TYPE:      Journal; Article; (JOURNAL ARTICLE)
LANGUAGE:           English
FILE SEGMENT:       Priority Journals
ENTRY MONTH:        200302
ENTRY DATE:         Entered STN: 20020918
                    Last Updated on STN: 20030212
                    Entered Medline: 20030211
AB     Escherichia blattae non-specific acid phosphatase (EB-NSAP) possesses a pyrophosphate-
       nucleoside phosphotransferase activity, which is C-5'-position selective.  Current
       mutational and structural data were used to generate a mutant EB-NSAP for a potential
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industrial application as an effective and economical protein catalyst in synthesizing nucleotides from nucleosides. First, Gly74 and Ile153 were replaced by Asp and Thr, respectively, since the corresponding replacements in the homologous enzyme from Morganella morganii reduced the K(m) value for inosine and thus increased the productivity of 5'-IMP. We determined the crystal structure of G74D/I153T, which has a reduced K(m) value for inosine, as expected. The tertiary structure of G74D/I153T was virtually identical to that of the wild-type. In addition, neither of the introduced side chains of Asp74 and Thr153 is directly involved in the interaction with inosine in a hypothetical binding mode of inosine to EB-NSAP, although both residues are situated near a potential inosine-binding site. These findings suggested that a slight structural change caused by an amino acid replacement around the potential inosine-binding site could significantly reduce the K(m) value. Prompted by this hypothesis, we designed several mutations and introduced them to G74D/I153T, to decrease the K(m) value further. This strategy produced a S72F/G74D/I153T mutant with a 5.4-fold lower K(m) value and a 2.7-fold higher V(max) value as compared to the wild-type EB-NSAP.

L8 ANSWER 3 OF 4 CAPLUS COPYRIGHT 2005 ACS on STN
ACCESSION NUMBER: 2001:185898 CAPLUS Full-text
DOCUMENT NUMBER: 134:233616
TITLE: Nucleoside-5'-phosphate producing enzyme mutants with enhanced activity designed from x-ray crystal structure analysis
INVENTOR(S): Ishikawa, Kohki; Suzuki, Ei-ichiro; Gondoh, Keiko; Shimba, Nobuhisa; Mihara, Yasuhiro; Kawasaki, Hisashi; Kurahashi, Osamu; Kouda, Tohru; Shimaoka, Megumi; Kozutsumi, Rie; Asano, Yasuhisa
PATENT ASSIGNEE(S): Ajinomoto Co., Inc., Japan
SOURCE: PCT Int. Appl., 150 pp.
CODEN: PIXXD2
DOCUMENT TYPE: Patent
LANGUAGE: Japanese
FAMILY ACC. NUM. COUNT: 1
PATENT INFORMATION:

PATENT NO.	KIND	DATE	APPLICATION NO.	DATE
WO 2001018184	A1	20010315	WO 2000-JP5973	20000901
W: AE, AG, AL, AM, AT, AU, AZ, BA, BB, BG, BR, BY, BZ, CA, CH, CN, CR, CU, CZ, DE, DK, DM, DZ, EE, ES, FI, GB, GD, GE, GH, GM, HR, HU, ID, IL, IN, IS, KE, KG, KP, KR, KZ, LC, LK, LR, LS, LT, LU, LV, MA, MD, MG, MK, MN, MW, MX, MZ, NO, NZ, PL, PT, RO, RU, SD, SE, SG, SI, SK, SL, TJ, TM, TR, TT, TZ, UA, UG, US, UZ, VN, YU, ZA, ZW, AM, AZ, BY, KG, KZ, MD, RU, TJ, TM				
RW: GH, GM, KE, LS, MW, MZ, SD, SL, SZ, TZ, UG, ZW, AT, BE, CH, CY, DE, DK, ES, FI, FR, GB, GR, IE, IT, LU, MC, NL, PT, SE, BF, BJ, CF, CG, CI, CM, GA, GN, GW, ML, MR, NE, SN, TD, TG				
JP 2001136984	A2	20010522	JP 2000-262120	20000831
BR 2000007056	A	20010814	BR 2000-7056	20000901
PRIORITY APPLN. INFO.:			JP 1999-249545 A	19990903
			WO 2000-JP5973 W	20000901

AB A variant nucleoside-5'-phosphate producing enzymes (nucleoside-5'- phosphate synthase) having an elevated nucleoside-5'-phosphate production activity, phosphotransferase activity and/or phosphatase activity, are disclosed. By identifying variations on the basis of x-ray structural anal. of known enzyme crystals, it is found out that the above enzyme has a structure wherein, in the nucleoside-5'-phosphate producing enzyme, a Lys residue, two Arg residues and two His residues are present, the Cα distances among these residues fall within a specific range, and there is a space allowing the attachment of nucleoside around these residues. Acid phosphatase (AP) from Escherichia blattae, other Escherichia species, Morganella, Providencia, Enterobacter, or Klebsiella, can be used for x-ray crystal structure anal. Preparation of nucleotidase activity acid phosphatase mutants of Escherichia blattae strain JCM1650, Morganella morganii, and Enterobacter aerogenes by substitution at Gly74Asp, Ile153Thr, or at other defined positions such as Ser72, was shown. Enhanced 5'-inosinic acid production and phosphate transfer activity, accompanies by lower Km values for inosine, and compared with that of wild-type and the mutant enzymes was also demonstrated. Atomic coordinates data from the X-ray crystal structure of AP complexed with molybdic acid (molybdate) was used for anal. and design. A process for efficiently and economically producing a nucleoside-5'-phosphate using the mutant enzyme is claimed.
REFERENCE COUNT: 7 THERE ARE 7 CITED REFERENCES AVAILABLE FOR THIS RECORD. ALL CITATIONS AVAILABLE IN THE RE FORMAT

L8 ANSWER 4 OF 4 MEDLINE on STN DUPLICATE 2
ACCESSION NUMBER: 2000296667 MEDLINE Full-text
DOCUMENT NUMBER: PubMed ID: 10835340
TITLE: X-ray structures of a novel acid phosphatase from Escherichia blattae and its complex with the transition-state analog molybdate.
AUTHOR: Ishikawa K; Mihara Y; Gondoh K; Suzuki E; Asano Y
CORPORATE SOURCE: Central Research Laboratories, Ajinomoto Co., Inc., 1-1 Suzuki-cho, Kawasaki-ku, Kawasaki 210-8681, Japan.
SOURCE: EMBO journal, (2000 Jun 1) 19 (11) 2412-23.
Journal code: 8208664. ISSN: 0261-4189.
PUB. COUNTRY: ENGLAND: United Kingdom
DOCUMENT TYPE: Journal; Article; (JOURNAL ARTICLE)
LANGUAGE: English
FILE SEGMENT: Priority Journals
ENTRY MONTH: 200007
ENTRY DATE: Entered STN: 20000728
Last Updated on STN: 20000728
Entered Medline: 20000720

AB The structure of Escherichia blattae non-specific acid phosphatase (EB-NSAP) has been determined at 1.9 A resolution with a bound sulfate marking the phosphate-binding site. The enzyme is a 150 kDa homohexamer. EB-NSAP shares a conserved sequence motif not only with several lipid phosphatases and the mammalian glucose-6- phosphatases, but also with the vanadium-containing chloroperoxidase (CPO) of Curvularia inaequalis. Comparison of the crystal structures of EB-NSAP and CPO reveals striking similarity in the active site structures. In addition, the topology of the EB-NSAP core shows considerable similarity to the fold of the active site containing part of the monomeric 67 kDa CPO, despite the lack of further sequence identity. These two enzymes are apparently related by divergent evolution. We have also determined the crystal structure of EB-NSAP complexed with the transition-state analog molybdate. Structural comparison of the native enzyme and the enzyme-molybdate complex reveals that the side-chain of His150, a putative catalytic residue, moves toward the molybdate so that it forms a hydrogen bond with the metal oxyanion when the molybdenum forms a covalent bond with NE2 of His189.

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=> s phosphatase and aerogenes and mut?
L9            6 FILE MEDLINE
L10          10 FILE CAPLUS
L11           8 FILE SCISEARCH
L12           1 FILE LIFESCI
L13           2 FILE BIOSIS
L14           2 FILE EMBASE

TOTAL FOR ALL FILES
L15          29 PHOSPHATASE AND AEROGENES AND MUT?

=> s l15 not 2001-2005
L16           6 FILE MEDLINE
L17          10 FILE CAPLUS
L18           8 FILE SCISEARCH
L19           1 FILE LIFESCI
L20           2 FILE BIOSIS
L21           2 FILE EMBASE

TOTAL FOR ALL FILES
L22          29 L15 NOT 2001-2005

=> dup rem l22
PROCESSING COMPLETED FOR L22
L23          20 DUP REM L22 (9 DUPLICATES REMOVED)

=> d ibib abs 1-20

L23 ANSWER 1 OF 20 SCISEARCH COPYRIGHT (c) 2005 The Thomson Corporation on
    STN
ACCESSION NUMBER: 2004:92187 SCISEARCH Full-text
THE GENUINE ARTICLE: 763RY
TITLE: Growth of Escherichia coli coexpressing phosphotriesterase
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and glycerophosphodiester phosphodiesterase, using paraoxon as the sole phosphorus source

AUTHOR: McLoughlin S Y; Jackson C; Liu J W; Ollis D L (Reprint)

CORPORATE SOURCE: Australian Natl Univ, Res Sch Chem, Bldg 35, Sci Rd, Canberra, ACT 0200, Australia (Reprint); Australian Natl Univ, Res Sch Chem, Canberra, ACT 0200, Australia

COUNTRY OF AUTHOR: Australia

SOURCE: APPLIED AND ENVIRONMENTAL MICROBIOLOGY, (JAN 2004) Vol. 70, No. 1, pp. 404-412.
Publisher: AMER SOC MICROBIOLOGY, 1752 N ST NW, WASHINGTON, DC 20036-2904 USA.
ISSN: 0099-2240.

DOCUMENT TYPE: Article; Journal

LANGUAGE: English

REFERENCE COUNT: 49

ABSTRACT IS AVAILABLE IN THE ALL AND IALL FORMATS

AB Phosphotriesterases catalyze the hydrolytic detoxification of phosphotriester pesticides and chemical warfare nerve agents with various efficiencies. The directed evolution of phosphotriesterases to enhance the breakdown of poor substrates is desirable for the purposes of bioremediation. A limiting factor in the identification of phosphotriesterase mutants with increased activity is the ability to effectively screen large mutant libraries. To this end, we have investigated the possibility of coupling phosphotriesterase activity to cell growth by using methyl paraoxon as the sole phosphorus source. The catabolism of paraoxon to phosphate would occur via the stepwise enzymatic hydrolysis of paraoxon to dimethyl phosphate, methyl phosphate, and then phosphate. The Escherichia coli strain DH10B expressing the phosphotriesterase from Agrobacterium radiobacter P230 (OpdA) is unable to grow when paraoxon is used as the sole phosphorus source. Enterobacter aerogenes is an organism capable of growing when dimethyl phosphate is the sole phosphorus source. The enzyme responsible for hydrolyzing dimethyl phosphate has been previously characterized as a nonspecific phosphohydrolase. We isolated and characterized the genes encoding the phosphohydrolase operon. The operon was identified from a shotgun clone that enabled E. coli to grow when dimethyl phosphate is the sole phosphorus source. E. coli coexpressing the phosphohydrolase and OpdA grew when paraoxon was the sole phosphorus source. By constructing a short degradative pathway, we have enabled E. coli to use phosphotriesters as a sole source of phosphorus.

L23 ANSWER 2 OF 20 CAPLUS COPYRIGHT 2005 ACS on STN

ACCESSION NUMBER: 2002:19321 CAPLUS Full-text

DOCUMENT NUMBER: 136:84776

TITLE: Enzymic method of nucleoside-5'-phosphate

INVENTOR(S): Iida, Iwao; Arashida, Takaki; Abe, Shigemitsu

PATENT ASSIGNEE(S): Ajinomoto Co., Inc., Japan

SOURCE: Jpn. Kokai Tokkyo Koho, 10 pp.
CODEN: JKXXAF

DOCUMENT TYPE: Patent

LANGUAGE: Japanese

FAMILY ACC. NUM. COUNT: 1

PATENT INFORMATION:

PATENT NO.	KIND	DATE	APPLICATION NO.	DATE
JP 2002000289	A2	20020108	JP 2000-189226	20000623

PRIORITY APPLN. INFO.: JP 2000-189226 20000623

OTHER SOURCE(S): CASREACT 136:84776

AB Nucleosides, especially low-solubility nucleosides, or their precursor crystal is phys. pulverized to a size having sp. surface area of 0.4 m2/g, incubated with enzyme such as acidic phosphatase in the presence of an phosphate donor to prepare nucleoside-5'-phosphate. Manufacture of 5'-guanylic acid from guanosine crystal in the presence of pyrophosphoric acid with acidic phosphatase mutant of Escherichia blattae was shown.

L23 ANSWER 3 OF 20 CAPLUS COPYRIGHT 2005 ACS on STN

ACCESSION NUMBER: 2001:185898 CAPLUS Full-text

DOCUMENT NUMBER: 134:233616

TITLE: Nucleoside-5'-phosphate producing enzyme mutants with enhanced activity designed from x-ray crystal structure analysis

INVENTOR(S): Ishikawa, Kohki; Suzuki, Ei-ichiro; Gondoh, Keiko; Shimba, Nobuhisa; Mihara, Yasuhiro; Kawasaki, Hisashi;

Kurahashi, Osamu; Kouda, Tohru; Shimaoka, Megumi; Kozutsumi, Rie; Asano, Yasuhisa
PATENT ASSIGNEE(S): Ajinomoto Co., Inc., Japan
SOURCE: PCT Int. Appl., 150 pp.
CODEN: PIXXD2
DOCUMENT TYPE: Patent
LANGUAGE: Japanese
FAMILY ACC. NUM. COUNT: 1
PATENT INFORMATION:

PATENT NO.	KIND	DATE	APPLICATION NO.	DATE
WO 2001018184	A1	20010315	WO 2000-JP5973	20000901
W: AE, AG, AL, AM, AT, AU, AZ, BA, BB, BG, BR, BY, BZ, CA, CH, CN, CR, CU, CZ, DE, DK, DM, DZ, EE, ES, FI, GB, GD, GE, GH, GM, HR, HU, ID, IL, IN, IS, KE, KG, KP, KR, KZ, LC, LK, LR, LS, LT, LU, LV, MA, MD, MG, MK, MN, MW, MX, MZ, NO, NZ, PL, PT, RO, RU, SD, SE, SG, SI, SK, SL, TJ, TM, TR, TT, TZ, UA, UG, US, UZ, VN, YU, ZA, ZW, AM, AZ, BY, KG, KZ, MD, RU, TJ, TM				
RW: GH, GM, KE, LS, MW, MZ, SD, SL, SZ, TZ, UG, ZW, AT, BE, CH, CY, DE, DK, ES, FI, FR, GB, GR, IE, IT, LU, MC, NL, PT, SE, BF, BJ, CF, CG, CI, CM, GA, GN, GW, ML, MR, NE, SN, TD, TG				
JP 2001136984	A2	20010522	JP 2000-262120	20000831
BR 2000007056	A	20010814	BR 2000-7056	20000901

PRIORITY APPLN. INFO.: JP 1999-249545 A 19990903
WO 2000-JP5973 W 20000901

AB A variant nucleoside-5'-phosphate producing enzymes (nucleoside-5'- phosphate synthase) having an elevated nucleoside-5'-phosphate production activity, phosphotransferase activity and/or phosphatase activity, are disclosed. By identifying variations on the basis of x-ray structural anal. of known enzyme crystals, it is found out that the above enzyme has a structure wherein, in the nucleoside-5'-phosphate producing enzyme, a Lys residue, two Arg residues and two His residues are present, the Cα distances among these residues fall within a specific range, and there is a space allowing the attachment of nucleoside around these residues. Acid phosphatase (AP) from Escherichia blattae, other Escherichia species, Morganella, Providencia, Enterobacter, or Klebsiella, can be used for x-ray crystal structure anal. Preparation of nucleotidase activity acid phosphatase mutants of Escherichia blattae strain JCM1650, Morganella morganii, and Enterobacter aerogenes by substitution at Gly74Asp, Ile153Thr, or at other defined positions such as Ser72, was shown. Enhanced 5'-inosinic acid production and phosphate transfer activity, accompanies by lower Km values for inosine, and compared with that of wild-type and the mutant enzymes was also demonstrated. Atomic coordinates data from the X-ray crystal structure of AP complexed with molybdic acid (molybdate) was used for anal. and design. A process for efficiently and economically producing a nucleoside-5'-phosphate using the mutant enzyme is claimed.

REFERENCE COUNT: 7 THERE ARE 7 CITED REFERENCES AVAILABLE FOR THIS RECORD. ALL CITATIONS AVAILABLE IN THE RE FORMAT

L23 ANSWER 4 OF 20 CAPLUS COPYRIGHT 2005 ACS on STN
ACCESSION NUMBER: 2001:11562 CAPLUS Full-text
DOCUMENT NUMBER: 135:89641
TITLE: Alternative pathways for siroheme synthesis in Klebsiella aerogenes
AUTHOR(S): Kolko, M. Miriam; Kapetanovich, Lori A.; Lawrence, Jeffrey G.
CORPORATE SOURCE: Department of Biological Sciences, University of Pittsburgh, Pittsburgh, PA, 15260, USA
SOURCE: Journal of Bacteriology (2001), 183(1), 328-335
CODEN: JOBAAY; ISSN: 0021-9193
PUBLISHER: American Society for Microbiology
DOCUMENT TYPE: Journal
LANGUAGE: English

AB Siroheme, the cofactor for sulfite and nitrite reductases, is formed by methylation, oxidation, and iron insertion into the tetrapyrrole uroporphyrinogen III (Uro-III). The CysG protein performs all three steps of siroheme biosynthesis in the enteric bacteria Escherichia coli and Salmonella enterica. In either taxon, cysG mutants cannot reduce sulfite to sulfide and require a source of sulfide or cysteine for growth. In addition, CysG-mediated methylation of Uro-III is required for de novo synthesis of cobalamin (coenzyme B12) in S. enterica. We have determined that cysG mutants of the related enteric bacterium Klebsiella aerogenes have no defect in the reduction of sulfite to sulfide. These data suggest that an alternative enzyme allows for siroheme biosynthesis in CysG-deficient strains of Klebsiella. However, Klebsiella cysG mutants fail to synthesize

coenzyme B12, suggesting that the alternative siroheme biosynthetic pathway proceeds by a different route. Gene cysF, encoding an alternative siroheme synthase homologous to CysG, has been identified by genetic anal. and lies within the cysFDNC operon; the cysF gene is absent from the E. coli and S. enterica genomes. While CysG is coregulated with the siroheme-dependent nitrite reductase, the cysF gene is regulated by sulfur starvation. Models for alternative regulation of the CysF and CysG siroheme synthases in Klebsiella and for the loss of the cysF gene from the ancestor of E. coli and S. enterica are presented.

REFERENCE COUNT: 29 THERE ARE 29 CITED REFERENCES AVAILABLE FOR THIS RECORD. ALL CITATIONS AVAILABLE IN THE RE FORMAT

L23 ANSWER 5 OF 20 MEDLINE on STN DUPLICATE 1
ACCESSION NUMBER: 2000175236 MEDLINE Full-text
DOCUMENT NUMBER: PubMed ID: 10708587
TITLE: Cloning and characterization of the UDP-sugar hydrolase gene (ushA) of Enterobacter aerogenes IFO 12010.
AUTHOR: Lee K S; Song S B; Kim K E; Kim Y H; Kim S K; Kho B H; Ko D K; Choi Y K; Lee Y K; Kim C K; Kim Y C; Lim J Y; Kim Y; Min K H; Wanner B L
CORPORATE SOURCE: Research Center for Biomedicinal Resources (Bio-Med RRC), Pai-Chai University, Taejon, 302-735, Korea.. kslee@www.paichai.ac.kr
SOURCE: Biochemical and biophysical research communications, (2000 Mar 16) 269 (2) 526-31.
Journal code: 0372516. ISSN: 0006-291X.
PUB. COUNTRY: United States
DOCUMENT TYPE: Journal; Article; (JOURNAL ARTICLE)
LANGUAGE: English
FILE SEGMENT: Priority Journals
ENTRY MONTH: 200004
ENTRY DATE: Entered STN: 20000427
Last Updated on STN: 20000427
Entered Medline: 20000419

AB A bacterial alkaline phosphatase (BAP, the phoA gene product) is primarily responsible for the hydrolysis of the substrates 5-bromo-4-chloro-3-indolylphosphate-p-toluidine (XP) and p-nitrophenyl phosphate (pNPP). Using these substrates and an E. coli phoA mutant, we have cloned Enterobacter aerogenes genes conferring an XP(+) phenotype. Two types of clones were identified based on phenotypic tests and DNA sequences. One of them is a E. aerogenes phoA gene (XP(+), pNPP(+)) as expected; surprisingly the other one was found to be a ushA gene (XP(+), pNPP(-)), which encodes an UDP (uridine 5'-diphosphate)-sugar hydrolase. The E. aerogenes ushA gene shares high sequence identity with ushA of E. coli and the mutationally silent ushA0 gene of Salmonella typhimurium at both the nucleotide (over 79%) and amino acid (over 93%) levels. Expression of the E. aerogenes ushA gene in E. coli produced high level of UDP-sugar hydrolase, as confirmed by TLC (thin layer chromatography) analysis together with a presence of a strong band due to a XP hydrolysis on a polyacrylamide gel.

L23 ANSWER 6 OF 20 CAPLUS COPYRIGHT 2005 ACS on STN
ACCESSION NUMBER: 1998:504855 CAPLUS Full-text
DOCUMENT NUMBER: 129:186140
TITLE: Nucleoside-5'-phosphate and its enzymic production with microbial acid phosphatase and mutants
INVENTOR(S): Mihara, Yasuhiro; Utagawa, Takashi; Yamada, Hideaki; Asano, Yasuhisa
PATENT ASSIGNEE(S): Ajinomoto Co., Inc., Japan
SOURCE: Jpn. Kokai Tokkyo Koho, 44 pp.
CODEN: JKXXAF
DOCUMENT TYPE: Patent
LANGUAGE: Japanese
FAMILY ACC. NUM. COUNT: 1
PATENT INFORMATION:

PATENT NO.	KIND	DATE	APPLICATION NO.	DATE
JP 10201481	A2	19980804	JP 1997-161674	19970618
EP 857788	A2	19980812	EP 1997-309365	19971120
EP 857788	A3	19991215		
EP 857788	B1	20030423		

R: AT, BE, CH, DE, DK, ES, FR, GB, GR, IT, LI, LU, NL, SE, MC, PT, IE, SI, LT, LV, FI, RO

ES 2199330	T3	20040216	ES 1997-309365	19971120
CN 1184157	A	19980610	CN 1997-122934	19971121
CN 1117870	B	20030813		
BR 9705813	A	19990427	BR 1997-5813	19971121
US 6015697	A	20000118	US 1997-975698	19971121
US 6207435	B1	20010327	US 1999-417090	19991013
US 2002004590	A1	20020110	US 2000-727578	20001204
US 6355472	B2	20020312		

PRIORITY APPLN. INFO.:

JP 1996-311103	A	19961121
JP 1997-161674	A	19970618
US 1997-975698	A3	19971121
US 1999-417090	A3	19991013

AB Disclosed is a method for efficiently producing nucleoside-5'-phosphates, which method comprises treating a nucleoside and a phosphoric acid donor at pH 3.0-5.5, with an acidic phosphatase or mutants with improved substrate affinity (Km <100) and stability. The enzyme has been produced from Morganella morganii, Escherichia blattae, Providencia stuartii, Enterobacter aerogenes, Klebsiella planticola, and Serratia ficaria, and their encoding DNA are isolated. Preparation of nucleotidase activity-low acidic phosphatase mutants of Escherichia blattae strain JCM1650 by substitution at 74-Gly→Asp, 153-Ile→Thr, 74-Gly→Asp and 153-Ile→Thr, or at other defined positions was shown. Production of 5'-inosinic acid, 5'-guanylic acid, 5'-uridylic acid, and 5'-cytidylic acid with the wild-type and the mutant enzymes was also demonstrated.

L23 ANSWER 7 OF 20 SCISEARCH COPYRIGHT (c) 2005 The Thomson Corporation on STN

ACCESSION NUMBER: 97:523729 SCISEARCH Full-text
THE GENUINE ARTICLE: XJ207
TITLE: Structure/function analysis of the PII signal transduction protein of Escherichia coli: Genetic separation of interactions with protein receptors
AUTHOR: Jiang P; Zucker P; Atkinson M R; Kamberov E S; Tirasophon W; Chandran P; Schefke B R; Ninfa A J (Reprint)
CORPORATE SOURCE: UNIV MICHIGAN, DEPT BIOL CHEM, SCH MED, 1301 E CATHERINE, ANN ARBOR, MI 48109 (Reprint); UNIV MICHIGAN, DEPT BIOL CHEM, SCH MED, ANN ARBOR, MI 48109
COUNTRY OF AUTHOR: USA
SOURCE: JOURNAL OF BACTERIOLOGY, (JUL 1997) Vol. 179, No. 13, pp. 4342-4353.
Publisher: AMER SOC MICROBIOLOGY, 1325 MASSACHUSETTS AVENUE, NW, WASHINGTON, DC 20005-4171.
ISSN: 0021-9193.
DOCUMENT TYPE: Article; Journal
FILE SEGMENT: LIFE
LANGUAGE: English
REFERENCE COUNT: 53

ABSTRACT IS AVAILABLE IN THE ALL AND IALL FORMATS

AB The PII protein, encoded by glnB, is known to interact with three bifunctional signal transducing enzymes (uridylyltransferase/uridylyl- removing enzyme, adenylyltransferase, and the kinase/phosphatase nitrogen regulator II [NRII or NtrB]) and three small-molecule effectors, glutamate, 2-ketoglutarate, and ATP. We constructed 15 conservative alterations of PII by site-specific mutagenesis of glnB and also isolated three random glnB mutants affecting nitrogen regulation. The abilities of the 18 altered PII proteins to interact with the PII receptors and the small-molecule effecters 2-ketoglutarate and ATP were examined by using purified components, Results with certain mutants suggested that the specificity for the various protein receptors was altered; other mutations affected the interaction with all three receptors and the small-molecule effectors to various extents, The apex of the large solvent-exposed T loop of the PII protein (P. D. Carr, E. Cheah, P. M. Suffolk, S. G. Vasudevan, N. E. Dixon, and D. L. Ollis, Acta Crytallogr. Sect. D 52:93-104, 1996), which includes the site of PII modification, was not required for the binding of small-molecule effecters but was necessary for the interaction with all three receptors, Mutations altering residues of this loop or affecting the nearby B loop of PII, which line a cleft between monomers in the trimeric PII, affected the interactions with protein receptors and the binding of small-molecule ligands, Thus, our results support the predictions made from structural studies that the exposed loops of PII and cleft formed at their interface are the sites of regulatory interactions.

L23 ANSWER 8 OF 20 SCISEARCH COPYRIGHT (c) 2005 The Thomson Corporation on STN
ACCESSION NUMBER: 97:188189 SCISEARCH Full-text
THE GENUINE ARTICLE: WK479
TITLE: Manganese(II) active site mutants of 3,4-dihydroxyphenylacetate 2,3-dioxygenase from Arthrobacter globiformis strain CM-2
AUTHOR: Boldt Y R; Whiting A K; Wagner M L; Sadowsky M J; Que L; Wackett L P (Reprint)
CORPORATE SOURCE: UNIV MINNESOTA, DEPT BIOCHEM, GORTNER LAB 140, ST PAUL, MN 55108 (Reprint); UNIV MINNESOTA, DEPT BIOCHEM, GORTNER LAB 140, ST PAUL, MN 55108; UNIV MINNESOTA, DEPT SOIL WATER & CLIMATE, ST PAUL, MN 55108; UNIV MINNESOTA, BIOL PROC TECHNOL INST, ST PAUL, MN 55108; UNIV MINNESOTA, CTR BIODEGRADAT RES & INFORMAT, ST PAUL, MN 55108; UNIV MINNESOTA, DEPT MICROBIOL, MINNEAPOLIS, MN 55455; UNIV MINNESOTA, DEPT CHEM, MINNEAPOLIS, MN 55455; UNIV MINNESOTA, CTR MET BIOCATALYSIS, MINNEAPOLIS, MN 55455
COUNTRY OF AUTHOR: USA
SOURCE: BIOCHEMISTRY, (25 FEB 1997) Vol. 36, No. 8, pp. 2147-2153. Publisher: AMER CHEMICAL SOC, 1155 16TH ST, NW, WASHINGTON, DC 20036. ISSN: 0006-2960.
DOCUMENT TYPE: Article; Journal
FILE SEGMENT: LIFE
LANGUAGE: English
REFERENCE COUNT: 45

ABSTRACT IS AVAILABLE IN THE ALL AND IALL FORMATS

AB Whereas all other members of the extradiol-cleaving catechol dioxygenase family are iron-dependent, the 3,4-dihydroxyphenylacetate 2,3-dioxygenase (MndD) from Arthrobacter globiformis CM-2 is dependent on manganese for catalytic activity. Recently, the endogenous iron ligands of one family member, the 2,3-dihydroxybiphenyl 1,2-dioxygenase (BphC), were identified crystallographically as two histidines and a glutamic acid [Sugiyama, K., et al. (1995) Proc. Japan Acad., Ser. B 71, 32-35; Han, et al. (1995) Science 270, 976-980; Senda, T., er al. (1996) J. Mel. Biol. 255, 735-752]. Though BphC and MndD have low overall sequence identity (23%), the three BphC metal ligands are all conserved in MndD (H155, H214, and E266). In order to determine whether these residues also act as ligands to manganese in MndD, site-directed mutants of each were constructed, purified, and analyzed for activity and metal content. Mutations H155A, H214A, and E266Q yielded purified enzymes with specific activities of <0.1% of that of the wild-type dioxygenase and bound 0.4, 1.8, and 33% of the wild-type level of manganese, respectively. The relatively high level of manganese [with a Mn(II) EPR signal distinctly different from that of the wild-type enzyme] observed for E266Q suggests that the glutamine may act as a weak ligand to the metal. Mutant E266D, which retains the potential metal binding capability of a carboxylate group, exhibited 12% of the wild-type activity in crude extracts, suggesting that Mn remains bound; however, this mutant protein was too unstable to be purified and analyzed for metal content. On the basis of the low activity and metal content of mutant proteins, we propose that the conserved residues H155, H214, and E266 ligate manganese in MndD. As is the case with the superoxide dismutases, the extradiol-cleaving catechol dioxygenases appear to utilize identical coordinating residues for their iron- and manganese-dependent enzymes.

L23 ANSWER 9 OF 20 CAPLUS COPYRIGHT 2005 ACS on STN
ACCESSION NUMBER: 1997:61305 CAPLUS Full-text
DOCUMENT NUMBER: 126:72040
TITLE: Nucleoside-5'-phosphate and its enzymic production with microbial acid phosphatase
INVENTOR(S): Mihara, Yasuhiro; Utagawa, Takashi; Yamada, Hideaki; Asano, Yasuhisa
PATENT ASSIGNEE(S): Ajinomoto Co., Inc., Japan
SOURCE: PCT Int. Appl., 94 pp. CODEN: PIXXD2
DOCUMENT TYPE: Patent
LANGUAGE: Japanese
FAMILY ACC. NUM. COUNT: 1
PATENT INFORMATION:

PATENT NO.	KIND	DATE	APPLICATION NO.	DATE

WO 9637603	A1	19961128	WO 1996-JP1402	19960524
W: BR, CA, CN, HU, JP, KR, PL, US, VN				
RW: AT, BE, CH, DE, DK, ES, FI, FR, GB, GR, IE, IT, LU, MC, NL, PT, SE				
JP 09037785	A2	19970210	JP 1996-94680	19960326
CA 2221774	AA	19961128	CA 1996-2221774	19960524
EP 832970	A1	19980401	EP 1996-914437	19960524
R: CH, DE, ES, FR, GB, IT, LI, NL				
CN 1191566	A	19980826	CN 1996-195770	19960524
CN 1105778	B	20030416		
JP 3180349	B2	20010625	JP 1996-535568	19960524
JP 2001245676	A2	20010911	JP 2000-395323	19960524
PL 183293	B1	20020628	PL 1996-323493	19960524
US 6010851	A	20000104	US 1997-750145	19970121
PRIORITY APPLN. INFO.:			JP 1995-149781 A	19950525
			JP 1996-94680 A	19960326
			JP 1996-535568 A3	19960524
			WO 1996-JP1402 W	19960524

AB A process for efficiently and economically producing a nucleoside-5'-phosphate which comprises treating a nucleoside and a phosphoric acid donor selected from the group consisting of poly-phosphoric acid (salts), phenylphosphoric acid (salts) and carbamyl phosphoric acid (salts) with an acid phosphatase, in particular the one having lowered nucleotidase activity, at pH 3.0.apprx.5.5. The enzyme has been produced from Morganella morganii, Escherichia blattae, Providencia stuartii, Enterobacter aerogenes, Klebsiella planticola, and Serratia ficaria, and their encoding DNA are isolated. The mutants of the enzyme with lowered nucleotidase activity can be obtained by site-specific mutation at, e.g., 72-Gly and/or 151-Ile of that of Morganella morganii. Production of 5'-inosinic acid, 5'-guanylic acid, 5'-uridylic acid, and 5'-cytidylic acid without nucleoside-2'-ester and nucleoside-3'-ester byproducts was shown.

L23 ANSWER 10 OF 20 SCISEARCH COPYRIGHT (c) 2005 The Thomson Corporation on STN
ACCESSION NUMBER: 96:831716 SCISEARCH Full-text
THE GENUINE ARTICLE: VT053
TITLE: BINUCLEAR METALLOHYDROLASES
AUTHOR: WILCOX D E (Reprint)
CORPORATE SOURCE: DARTMOUTH COLL, DEPT CHEM, HANOVER, NH, 03755 (Reprint)
COUNTRY OF AUTHOR: USA
SOURCE: CHEMICAL REVIEWS, (NOV 1996) Vol. 96, No. 7, pp. 2435-2458
ISSN: 0009-2665.
DOCUMENT TYPE: General Review; Journal
FILE SEGMENT: PHYS
LANGUAGE: ENGLISH
REFERENCE COUNT: 273

L23 ANSWER 11 OF 20 SCISEARCH COPYRIGHT (c) 2005 The Thomson Corporation on STN
ACCESSION NUMBER: 96:777931 SCISEARCH Full-text
THE GENUINE ARTICLE: VN917
TITLE: 2-METAL ION CATALYSIS IN ENZYMATIC ACYL-TRANSFER AND PHOSPHORYL-TRANSFER REACTIONS
AUTHOR: STRATER N; LIPSCOMB W N (Reprint); KLABUNDE T; KREBS B
CORPORATE SOURCE: HARVARD UNIV, DEPT CHEM & BIOL CHEM, 12 OXFORD ST, CAMBRIDGE, MA, 02138 (Reprint); HARVARD UNIV, DEPT CHEM & BIOL CHEM, CAMBRIDGE, MA, 02138; UNIV MUNSTER, INST ANORGAN CHEM, D-48149 MUNSTER, GERMANY
COUNTRY OF AUTHOR: USA; GERMANY
SOURCE: ANGEWANDTE CHEMIE-INTERNATIONAL EDITION IN ENGLISH, (07 OCT 1996) Vol. 35, No. 18, pp. 2024-2055.
ISSN: 0570-0833.
DOCUMENT TYPE: General Review; Journal
FILE SEGMENT: PHYS; LIFE
LANGUAGE: ENGLISH
REFERENCE COUNT: 476

L23 ANSWER 12 OF 20 SCISEARCH COPYRIGHT (c) 2005 The Thomson Corporation on STN
ACCESSION NUMBER: 93:664597 SCISEARCH Full-text
THE GENUINE ARTICLE: ME008

TITLE: MUTATIONAL ANALYSIS OF THE BACTERIAL SIGNAL-TRANSDUCING PROTEIN-KINASE PHOSPHATASE NITROGEN REGULATOR-II (NR(II) OR NTR(B))
AUTHOR: ATKINSON M R; NINFA A J (Reprint)
CORPORATE SOURCE: WAYNE STATE UNIV, SCH MED, DEPT BIOCHEM, DETROIT, MI, 48201
COUNTRY OF AUTHOR: USA
SOURCE: JOURNAL OF BACTERIOLOGY, (NOV 1993) Vol. 175, No. 21, pp. 7016-7023.
ISSN: 0021-9193.
DOCUMENT TYPE: Article; Journal
FILE SEGMENT: LIFE
LANGUAGE: ENGLISH
REFERENCE COUNT: 38

ABSTRACT IS AVAILABLE IN THE ALL AND IALL FORMATS

AB The signal-transducing kinase/phosphatase nitrogen regulator II (NR(II) or NtrB) is required for the efficient positive and negative regulation of glnA, encoding glutamine synthetase, and the Ntr regulon in response to the availability of ammonia. Alteration of highly conserved residues within the kinase/phosphatase domain of NR(II) revealed that the positive and negative regulatory functions of NR(II) could he genetically separated and that negative regulation hy NR(II) did not require the highly conserved His-139, Glu-140, Asn-248, Asp-287, Gly-289, Gly-291, Gly-313, or Gly-315 residue. These mutations affected the positive regulatory function of NR(II) to various extents. Certain substitutions at codons 139 and 140 resulted in mutant NR(II) proteins that were transdominant negative regulators of glnA and the Ntr regulon even in the absence of nitrogen limitation. In addition, we examined three small deletions near the 3' end of the gene encoding NR(II); these resulted in altered proteins that retained the negative regulatory function but were defective to various extents in the positive regulatory function. A truncated NR(II) protein missing the C-terminal 59 codons because of a nonsense mutation at codon 291 lacked entirely the positive regulatory function but was a negative regulator of glnA even in the absence of nitrogen limitation. Thus, we have identified both point and deletion mutations that convert NR(II) into a negative regulator of glnA and the Ntr regulon irrespective of the nitrogen status of the cell.

L23 ANSWER 13 OF 20 SCISEARCH COPYRIGHT (c) 2005 The Thomson Corporation on STN
ACCESSION NUMBER: 92:444950 SCISEARCH Full-text
THE GENUINE ARTICLE: JE399
TITLE: CHARACTERIZATION OF ESCHERICHIA-COLI GLNL MUTATIONS AFFECTING NITROGEN REGULATION
AUTHOR: ATKINSON M R; NINFA A J (Reprint)
CORPORATE SOURCE: WAYNE STATE UNIV, SCH MED, DEPT BIOCHEM, DETROIT, MI, 48201
COUNTRY OF AUTHOR: USA
SOURCE: JOURNAL OF BACTERIOLOGY, (JUL 1992) Vol. 174, No. 14, pp. 4538-4548.
ISSN: 0021-9193.
DOCUMENT TYPE: Article; Journal
FILE SEGMENT: LIFE
LANGUAGE: ENGLISH
REFERENCE COUNT: 46

ABSTRACT IS AVAILABLE IN THE ALL AND IALL FORMATS

AB Nitrogen regulator II (NR(II)), the product of the Escherichia coli glnL (ntrB) gene, regulates the activation of transcription of glnA and the Ntr regulon by catalyzing the phosphorylation and dephosphorylation of the transcription factor NR(I). Previous results have indicated that under conditions of nitrogen excess, transcriptional activation is prevented by an NR(I)-phosphate phosphatase activity that is observed when NR(II) and another signal transduction protein known as P(II) (the glnB product) interact. The availability of P(II) for this interaction is controlled by a uridylyltransferase/uridylyl-removing enzyme, encoded by glnD, that reversibly modifies P(II) in response to intracellular signals of nitrogen availability. Here we describe the isolation and characterization of missense mutations in glnL that suppress the Ntr- phenotype resulting from a leaky glnD mutation. The regulation of glnA expression in the pseudorevertants was found to vary from complete insensitivity to ammonia in some strains (GlnC phenotype) to nearly normal regulation by ammonia in other strains. Sequence analysis indicated that in 16 instances suppression was due to point mutations at 14 different sites; 10 different mutations resulting in a variety of phenotypes were identified in a cluster extending from codons 111 to 154 flanking the site of NR(II) autophosphorylation at His-139. Complementation experiments with

multicopy plasmids encoding NR(II) or P(II) showed that suppression by GlnC glnL alleles was eliminated upon introduction of the plasmid encoding NR(II) but was not affected by introduction of the plasmid encoding P(II). Conversely, suppression by certain glnL alleles that resulted in regulated expression of glnA was eliminated upon introduction of either the plasmid encoding NR(II) or that encoding P(II). We hypothesize that mutants of the latter type result in a subtle perturbation of the NR(II)-P(II) interaction and suggest two possible mechanisms for their effects.

L23 ANSWER 14 OF 20 MEDLINE on STN DUPLICATE 2
ACCESSION NUMBER: 90205629 MEDLINE Full-text
DOCUMENT NUMBER: PubMed ID: 2181242
TITLE: Molecular characterization of pulA and its product, pullulanase, a secreted enzyme of Klebsiella pneumoniae UNF5023.
AUTHOR: Kornacker M G; Pugsley A P
CORPORATE SOURCE: Unite de Genetique Moleculaire, Institut Pasteur, Paris, France.
SOURCE: Molecular microbiology, (1990 Jan) 4 (1) 73-85.
Journal code: 8712028. ISSN: 0950-382X.
PUB. COUNTRY: ENGLAND: United Kingdom
DOCUMENT TYPE: Journal; Article; (JOURNAL ARTICLE)
LANGUAGE: English
FILE SEGMENT: Priority Journals
OTHER SOURCE: GENBANK-X52181
ENTRY MONTH: 199005
ENTRY DATE: Entered STN: 19900601
Last Updated on STN: 19900601
Entered Medline: 19900509

AB The determined nucleotide sequence of the Klebsiella pneumoniae UNF5023 gene pulA comprises a single open reading frame coding for a 1090-residue precursor of the secreted protein pullulanase. The predicted sequence of this protein is highly homologous to that of pullulanase of Klebsiella aerogenes strain W70. However, the UNF5023 pullulanase lacks a collagen-like sequence present at the N-terminus of the mature W70 enzyme and differs further from the W70 pullulanase around residue 300 and at the C-terminus. Pullulanases with or without the collagen-like sequence could not be separated by gel electrophoresis under denaturing or non-denaturing conditions, and were unaffected by collagenase. A large central domain which is highly conserved in both UNF5023 and W70 polypeptides contains eight short sequences that are also found in amylases and iso-amylases. Linker mutations in the region of the UNF5023 pulA gene coding for this domain abolished catalytic activity without affecting transport of the polypeptide across the outer membrane. Hybrid proteins comprising at least the amino-terminal 656 residues of prepullulanase fused to alkaline phosphatase were partially localized to the cell surface, as judged by their accessibility to anti-pullulanase serum in immuno-fluorescence tests. On the basis of these results, we tentatively propose that secretion signals required for recognition and translocation across the outer membrane via the pullulanase-specific extension of the secretion pathway are located near the N-terminus of the pullulanase polypeptide.

L23 ANSWER 15 OF 20 MEDLINE on STN
ACCESSION NUMBER: 76167598 MEDLINE Full-text
DOCUMENT NUMBER: PubMed ID: 4459
TITLE: L-Asparaginase of Klebsiella aerogenes.
Activation of its synthesis by glutamine synthetase.
AUTHOR: Resnick A D; Magasanik B
SOURCE: Journal of biological chemistry, (1976 May 10) 251 (9) 2722-8.
Journal code: 2985121R. ISSN: 0021-9258.
PUB. COUNTRY: United States
DOCUMENT TYPE: Journal; Article; (JOURNAL ARTICLE)
LANGUAGE: English
FILE SEGMENT: Priority Journals
ENTRY MONTH: 197607
ENTRY DATE: Entered STN: 19900313
Last Updated on STN: 19980206
Entered Medline: 19760706

AB An L-asparaginase has been purified some 250-fold from extracts of Klebsiella aerogenes to near homogeneity. The enzyme has a molecular weight of 141,000 as measured by gel filtration and appears to consist of four subunits of molecular weight 37,000. The enzyme has high affinity for L-asparagine, with a Km below 10(-5) M, and hydrolyzes glutamine at

a 20-fold lower rate, with a Km of 10(-3) M. Interestingly, the enzyme exhibits marked gamma-glutamyltransferase activity but comparatively little beta-aspartyl-transferase activity. A mutant strain lacking this asparaginase has been isolated and grows at 1/2 to 1/3 the rate of the parent strain when asparagine is provided in the medium as the sole source of nitrogen. This strain grows as well as the wild type when the medium is supplemented with histidine or ammonia. Glutamine synthetase activates the formation of L-asparaginase. Mutants lacking glutamine synthetase fail to produce the asparaginase, and mutants with a high constitutive level of glutamine synthetase also contain the asparaginase at a high level. Thus, the formation of asparaginase is regulated in parallel with that of other enzymes capable of supplying the cell with ammonia or glutamate, such as histidase and proline oxidase. Formation of the asparaginase does not require induction by asparaginase and is not subject to catabolite repression.

L23 ANSWER 16 OF 20 MEDLINE on STN
ACCESSION NUMBER: 74268230 MEDLINE Full-text
DOCUMENT NUMBER: PubMed ID: 4366250
TITLE: Regulation of glycerol catabolism in Klebsiella aerogenes.
AUTHOR: Ruch F E; Lengeler J; Lin E C
SOURCE: Journal of bacteriology, (1974 Jul) 119 (1) 50-6.
Journal code: 2985120R. ISSN: 0021-9193.
PUB. COUNTRY: United States
DOCUMENT TYPE: Journal; Article; (JOURNAL ARTICLE)
LANGUAGE: English
FILE SEGMENT: Priority Journals
ENTRY MONTH: 197409
ENTRY DATE: Entered STN: 19900310
Last Updated on STN: 19900310
Entered Medline: 19740911

L23 ANSWER 17 OF 20 CAPLUS COPYRIGHT 2005 ACS on STN
ACCESSION NUMBER: 1971:49590 CAPLUS Full-text
DOCUMENT NUMBER: 74:49590
TITLE: Synthesis of exopolysaccharide by Klebsiella aerogenes membrane preparations and the involvement of lipid intermediates
AUTHOR(S): Sutherland, Ian W.; Norval, Mary
CORPORATE SOURCE: Dep. Gen. Microbiol., Univ. Edinburgh, Edinburgh, UK
SOURCE: Biochemical Journal (1970), 120(3), 567-76
CODEN: BIJOAK; ISSN: 0264-6021
DOCUMENT TYPE: Journal
LANGUAGE: English
AB Membrane prepns. from E. aerogenes type 8 transferred glucose and galactose from their UDP derivs. to a lipid and to polymer. The ratio of glucose to galactose transfer in both cases was 1:2. This is the same ratio in which these sugars occur in native polysaccharide. Galactose transfer was dependent on prior glucosylation of the lipid. Mutants were obtained lacking glucosyltransferase and galactosyltransferase. The transferase activities in a number of nonmucoid mutants was examined Glucose transfer was partially inhibited by UMP, and incorporation of either glucose or galactose into lipid was decreased in the presence of UDP. The sugars are thought to be linked to a lipid through a pyrophosphate bond, and treatment of the lipid intermediates with phenol yielded water-soluble compds. These could be dephosphorylated with alkaline phosphatase. Transfer of glucuronic acid to lipid or polymer from UDP-glucuronic acid was much lower than that of the other 2 sugars. The fate of sugars incorporated into polymer was also followed. Some conversion of glucose into galactose and glucuronic acid occurred. Mutants unable to transfer glucose or galactose to lipid were unable to form polymer. Other mutants capable of lipid glycosylation were in some cases unable to form polymer. A model for capsular polysaccharide synthesis is proposed and its similarity to the formation of other polymers outside the cell membrane is discussed.

L23 ANSWER 18 OF 20 MEDLINE on STN DUPLICATE 3
ACCESSION NUMBER: 65097591 MEDLINE Full-text
DOCUMENT NUMBER: PubMed ID: 14292996
TITLE: DEGRADATION OF INORGANIC POLYPHOSPHATE IN MUTANTS OF AEROBACTER AEROGENES.
AUTHOR: HAROLD F M; HAROLD R L
SOURCE: Journal of bacteriology, (1965 May) 89 1262-70.
Journal code: 2985120R. ISSN: 0021-9193.
PUB. COUNTRY: United States

DOCUMENT TYPE: Journal; Article; (JOURNAL ARTICLE)
LANGUAGE: English
FILE SEGMENT: OLDMEDLINE; NONMEDLINE
ENTRY MONTH: 199612
ENTRY DATE: Entered STN: 19990716
Last Updated on STN: 19990716
Entered Medline: 19961201

L23 ANSWER 19 OF 20 MEDLINE on STN DUPLICATE 4
ACCESSION NUMBER: 64129241 MEDLINE Full-text
DOCUMENT NUMBER: PubMed ID: 14171262
TITLE: ENZYMIC AND GENETIC CONTROL OF POLYPHOSPHATE ACCUMULATION IN AEROBACTER AEROGENES.
AUTHOR: HAROLD F M
SOURCE: Journal of general microbiology, (1964 Apr) 35 81-90.
Journal code: 0375371. ISSN: 0022-1287.
PUB. COUNTRY: ENGLAND: United Kingdom
DOCUMENT TYPE: Journal; Article; (JOURNAL ARTICLE)
LANGUAGE: English
FILE SEGMENT: OLDMEDLINE; NONMEDLINE
ENTRY MONTH: 199612
ENTRY DATE: Entered STN: 19990716
Last Updated on STN: 19990716
Entered Medline: 19961201

L23 ANSWER 20 OF 20 CAPLUS COPYRIGHT 2005 ACS on STN
ACCESSION NUMBER: 1964:449632 CAPLUS Full-text
DOCUMENT NUMBER: 61:49632
ORIGINAL REFERENCE NO.: 61:8656a-c
TITLE: The expression of genes of Escherichia coli in Serratia marcescens
AUTHOR(S): Levinthal, C.; Signer, E. R.; Torriani, A.
CORPORATE SOURCE: Massachusetts Inst. of Technol., Cambridge
SOURCE: Bulletin of the New York Academy of Medicine (1962), 38(5), 365
CODEN: BNYMAM; ISSN: 0028-7091
DOCUMENT TYPE: Journal
LANGUAGE: Unavailable

AB An episomal element carrying the genes for synthesis of β-galactosidase (lac+) and alkaline phosphatase (P+) in addition to the fertility factor was transferred from E. coli to a lac-- P- strain of S. marcescens (50 and 58 mole % guanine plus cytosine, resp.). The parental P+ S. marcescens produced an alkaline phosphatase similar to that from E. coli. However, its immunologic reaction and isoelec. pt. and the fingerprint of a tryptic digest of the purified protein were markedly different in the 2 enzymes. The enzyme produced by the E. coli gene functioning in a P- mutant of S. marcescens seemed identical with the E. coli phosphatase. The enzyme fingerprint from this hybrid cell contained all the tryptic peptides found in E. coli enzyme fingerprints. Apparently, the expression of structural information was independent of cytoplasmic environment. However, although only one of the 2 phosphate repressor genes was transferred on the episome, phosphatase synthesis was repressed under identical conditions in both the merozygote and E. coli. It is suggested that although structural information is species-specific, at least some regulatory information is less specific.

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